IN THE SPECIFICATION:

Please substitute the enclosed sequence listing for that previously filed.

At page 5, line 6 through page 6, line 16, please substitute the following:

BRIEF DESCRIPTION OF ~~THE DRAWINGS~~ PREFERRED EMBODIMENTS

~~FIG.~~ **EMBODIMENT 1**. Process for finding candidate tumor markers~~, using~~ uses fluorescent-PCR expression comparison (F-PEC). Genes over-expressed in tumors are mined from gene expression databases. A normalized cDNA panel is used to rapidly compare expression levels in malignant and normal tissues. The process requires an initial PCR to determine specificity of the primers, the product melting temperature and expression range of the tested samples. The highest expressing sample from the first PCR is serially diluted to create a standard curve for a second PCR, yielding information on the relative expression over several orders of magnitude.

~~FIGS.~~ **EMBODIMENT 2 (A-D).** Fluorescent-PCR ~~verification of~~ verified a candidate glioblastoma marker, *GPNMB*.

~~Fig.~~ **EMBODIMENT 2A.** Template cDNA from a bulk glioblastoma (GBM 861) and matched glioma/normal tissue pairs (GS1099/Cortex1099 and AA1100/Cortex1100) were amplified with primers specific for *GPNMB*.

~~Fig.~~ **EMBODIMENT 2B**. Melting curve analysis is performed simultaneously to optimize detection temperature, revealing a single peak consistent with a single amplification product.

~~Fig.~~ **EMBODIMENT 2C.** After fluorescent-PCR, all reaction products were visualized on an agarose gel to verify a single product of the correct size.

~~Fig.~~ **EMBODIMENT 2D.** Northern blot of normal fetal brain and three established GBM cell lines also show a difference in expression for *GPNMB*.

~~FIG.~~ **EMBODIMENT 3.** Relative expression of the tumor markers was determined in 12 high-grade astrocytomas, one glioblastoma cell line (D450-MG), and normal tissues. Glioblastoma (GBM), gliosarcoma (GS), anaplastic astrocytoma (AA) and cortex samples ~~with~~ from the same patient number ~~indicate~~ indicated matched normal/tumor pairs removed during the same surgery. Gene expression levels determined by fluorescent-PCR were plotted relative to the highest expression tumor in each case. Gene expression ~~is~~ was graphically displayed relative to serial dilutions of the highest expressing tumor.

~~FIG.~~ **EMBODIMENT 4 (A-B).** Western Blotting of Annexin A1 was performed to compare protein levels from brain tumors, glioblastoma cell lines and normal neural tissue.

~~Fig.~~ **EMBODIMENT 4A.** Expression in both glioblastoma cell lines (D392-MG, D450-MG & D534-MG) and primary GBM indicate that protein ~~expression~~ is expressed in transformed, but not normal (Cortex 1127, Cortex 1162 & Cortex 1421) tissues.

~~Fig.~~ **EMBODIMENT 4B.** Normal tissues from different normal brain regions did not express high levels of ANXA1 protein compared to a glioblastoma (GBM 1132) or an oligodendroglioma (Oligo 1330).